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## Restriction Map of the RSV G Gene

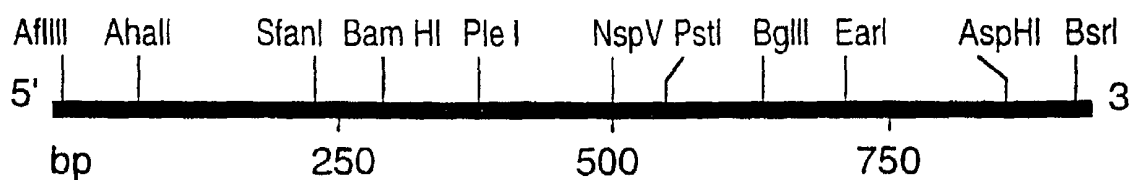


FIG.1



FIG.2A

10	19	28	37	46	55
TGCAAC ATG TOC AAA AAC AAG GAC CAA CGC ACC GCT AAG ACA CTA GAA AAG ACC					
Met Ser Lys Asn Lys Asp Gln Arg Thr Ala Lys Thr Leu Glu Lys Thr					
64	73	82	91	100	109
TGG GAC ACT CTC AAT CAT TTA TTA TTC ATA TCA TCG GGC TTA TAT AAG TTA AAT					
Trp Asp Thr Leu Asn His Leu Leu Phe Ile Ser Ser Gly Leu Tyr Lys Leu Asn					
118	127	136	145	154	163
CTT AAA TCT GTA GCA CAA ATC ACA TTA TOC ATT CTG GCA ATG ATA ATC TCA ACT					
Leu Lys Ser Val Ala Gln Ile Thr Leu Ser Ile Leu Ala Met Ile Ile Ser Thr					
172	181	190	199	208	217
TCA CTT ATA ATT ACA GCC ATC ATA TTC ATA GCC TCG GCA AAC CAC AAA GTC ACA					
Ser Leu Ile Ile Thr Ala Ile Ile Phe Ile Ala Ser Ala Asn His Lys Val Thr					
226	235	244	253	262	271
CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC CAG ATC AAG AAC ACA ACC CCA					
Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Ser Gln Ile Lys Asn Thr Thr Pro					
280	289	298	307	316	325
ACA TAC CTC ACT CAG GAT OCT CAG CTT GGA ATC AGC TTC TCC AAT CTG TCT GAA					
Thr Tyr Leu Thr Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser Asn Leu Ser Glu					



FIG.2B

334	343	352	361	370	379
ATT ACA TCA CAA ACC ACC ACC ATA GCT TCA ACA ACA GGA GTC AAG TCA					
Ile Thr Ser Gln Thr Thr Thr Ile Leu Ala Ser Thr Thr Pro Gly Val Lys Ser					
388	397	406	415	424	433
AAC CTG CAA CCC ACA ACA GTC AAG ACT AAA AAC ACA ACA ACC CAA ACA CAA					
Asn Leu Gln Pro Thr Thr Thr Val Lys Thr Lys Asn Thr Thr Thr Gln Thr Gln					
442	451	460	469	478	487
CCC AGC AAG CCC ACT ACA AAA CAA CAA CAA CCA CCA AAA AAA CCC AAT					
Pro Ser Lys Pro Thr Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn					
496	505	514	523	532	541
AAT GAT TTT CAC TTC GAA GTG TTT AAC TTT GTA CCC TGC AGC ATA TGC AGC AAC					
Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser Asn					
550	559	568	577	586	595
AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA CCA CCA CCA AAG					
Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys Pro Gly Lys					
604	613	622	631	640	
AAA ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA ACC AAA GAT					
Lys Thr Thr Thr Lys Pro Thr Thr Lys Lys Pro Thr Phe Lys Thr Thr Lys Lys Asp					

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## FIG. 2C

658	667	676	685	694	703
CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC AAG CCC ACA GAA					
Leu Lys Pro Gln Thr Thr Lys Pro Lys Pro Lys Glu Val Pro Thr Thr Lys Pro Thr Glu					
712	721	730	739	748	757
GAG CCA ACC ATC AAC ACC ACC AAA ACA AAC AAC ATC ACA ACT ACA CTG CTC ACC AAC					
Glu Pro Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr Thr Leu Leu Thr Asn					
766	775	784	793	802	811
AAC ACC ACA GGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC TTC CAC TCA ACC					
Asn Thr Thr Gly Asn Pro Lys Leu Thr Thr Ser Gln Met Glu Thr Phe His Ser Thr					
820	829	838	847	856	865
TCC TCC GAA GGC AAT CTA AGC CCT TCT CAA GTC TCC ACA ACA TCC GAG CAC CCA					
Ser Ser Glu Gly Asn Leu Ser Pro Ser Gln Val Ser Thr Thr Ser Glu His Pro					
874	883	892	901	914	
TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CCG CAG TAGTATTAA AAAAAAAAA					
Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln .					

FIG.3A

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CAC AAA GTC ACA CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC CAG ATC AAG	54
His Lys Val Thr Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys	18
AAC ACA ACC CCA ACA TAC CTC ACT CAG GAT CCT CAG CTT GGA ATC AGC TTC TTC	108
Asn Thr Thr Pro Thr Tyr Thr Leu Thr Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser	36
AAT CTG TCT GAA ATT ACA TCA CAA ACC ACC ATA GCT CTA GCT TCA ACA ACA CCA	162
Asn Leu Ser Glu Ile Thr Ser Gln Thr Thr Thr Ile Leu Ala Ser Thr Thr Pro	54
GGA GTC AAG TCA AAC CTG CAA CCC ACA ACA GTC AAG ACT AAA AAC ACA ACA ACA	216
Gly Val Lys Ser Asn Leu Gln Pro Thr Thr Thr Val Lys Thr Lys Asn Thr Thr Thr	72
ACC CAA ACA CCA CCC AGC AAG CCC ACT ACA AAA CAA CCG CAA AAC AAA CCA CCA	270
Thr Gln Thr Thr Gln Pro Ser Lys Pro Thr Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro	90
AAC AAA CCC AAT AAT GAT TTT CAC TTC GAA GIG TTT AAC TTT GTA CCC TGC AGC	324
Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser	108
ATA TGC AGC AAC AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA	378
Ile Cys Ser Asn Asn Pro Thr Cys Thr Ala Ile Cys Lys Arg Ile Pro Asn Lys	126
AAA CCA GGA AAG AAA ACC ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA	432
Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys Thr	144

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## FIG.3B

ACC AAA AAA GAT CTC AAA OCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC 486  
 Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr 162  
  
 AAG CCC ACA GAA GAG CCA ACC ATC AAC ACC ACC AAA ACA AAC ATC ACA ACT ACA 540  
 Lys Pro Thr Glu Glu Pro Thr Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr 180  
  
 CTG CTC ACC AAC AAC ACC ACA GGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC 594  
 Leu Leu Thr Asn Asn Thr Thr Gly Asn Pro Lys Leu Thr Ser Gln Met Glu Thr 198  
  
 TTC CAC TCA ACC TCC TCC GAA GGC AAT CTA AGC OCT TCT CAA GTC TCC ACA ACA 648  
 Phe His Ser Thr Ser Ser Glu Glu Asn Leu Ser Pro Ser Gln Val Ser Thr Thr 216  
  
 TCC GAG CAC CCA TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAG 699  
 Ser Glu His Pro Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln 232  
  
 TTATTTAA AAAAAAAAAA

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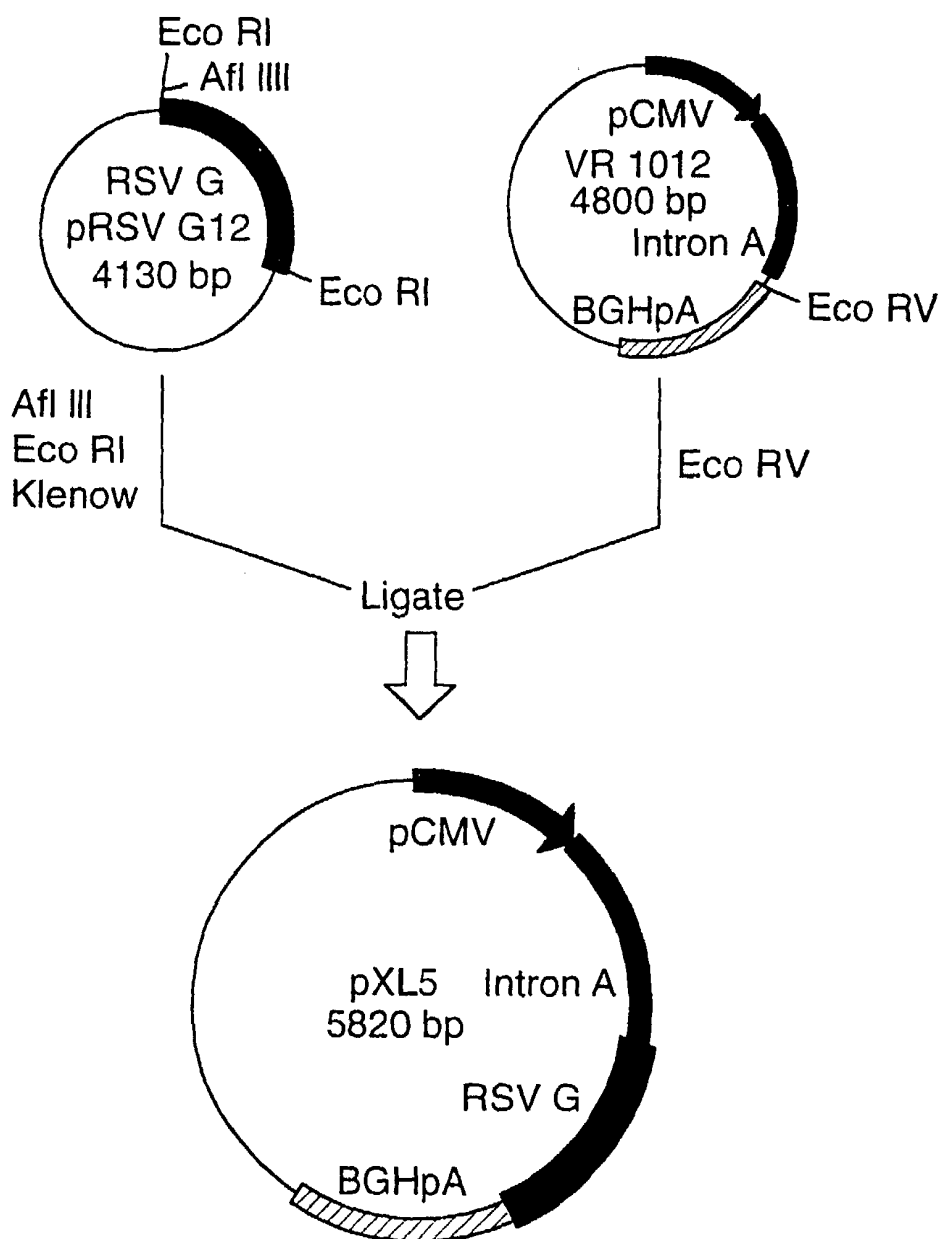


FIG.4.

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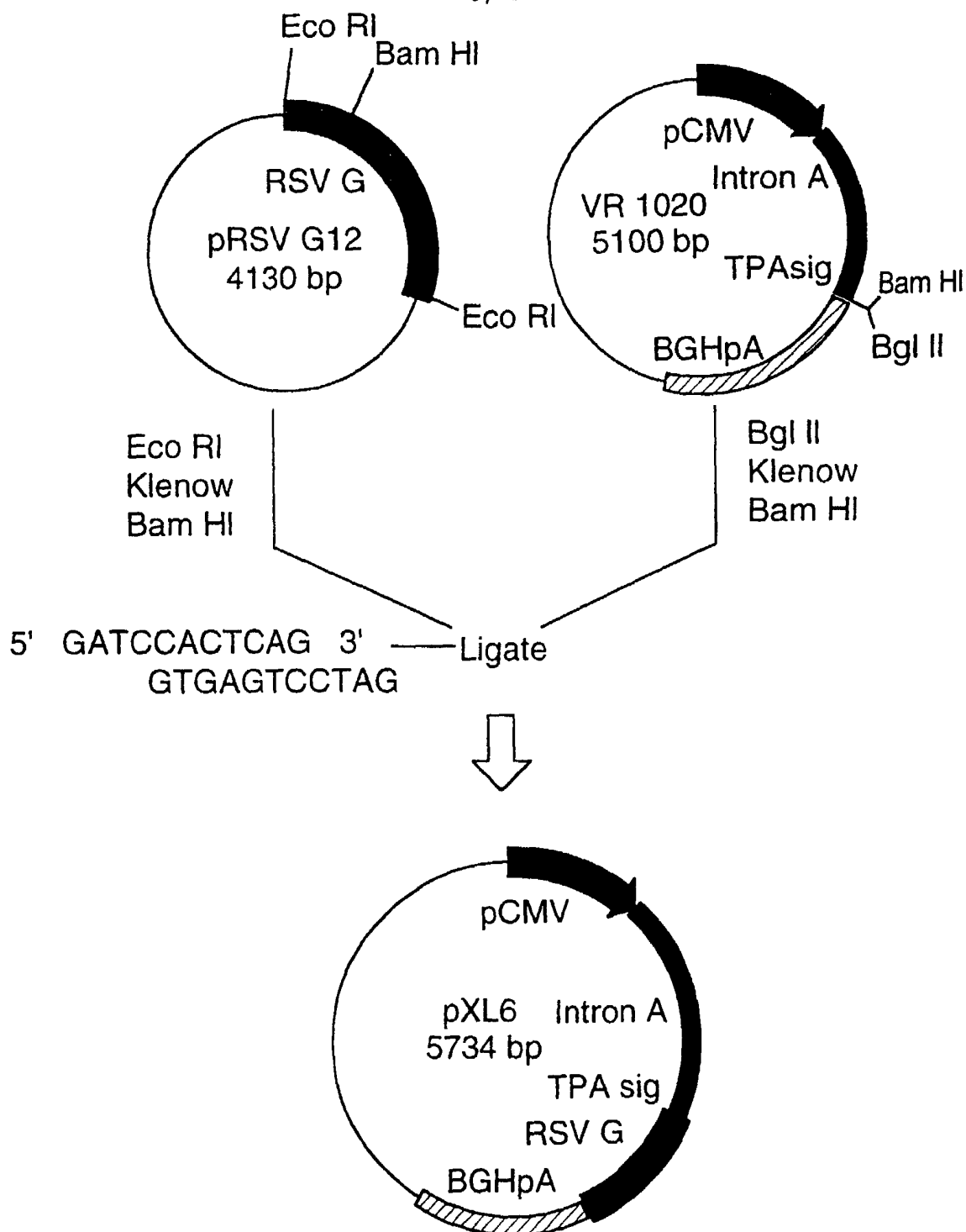


FIG.5



FIG.6A

10 20 30 40 50 60 70  
 TOGGCGGTTT CCGTATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT  
 80 90 100 110 120 130 140  
 GTAAAGCGGAT GCGGGAGCA GACAAGCCCG TCAGGCGCGG TCAGCGGGTG TTGGCGGGTG TOGGCGGCTGG  
 150 160 170 180 190 200 210  
 CTTAACTATG CCGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATCCG GGTGGAATA CCGCACAGAT  
 220 230 240 250 260 270 280  
 GGGTAAGGAG AAAATACCGC ATCAGATTGG CTATTGGCCA TTGCATACGT TGTATCCATA TCATAATAATG  
 290 300 310 320 330 340 350  
 TACATTATTA TTGGCICATG TCCAAACATTA CCGCCATGTT GACATTGATT ATTIGACTAGT TATTAAATAGT  
 360 370 380 390 400 410 420  
 AATCAATTAC GGGGICATTA GTTCATAGCC CATATATGGA GTTCCCGGTT ACATAACTTGA CCGPAAATGG  
 430 440 450 460 470 480 490  
 CCGGCGCTGC TCACCGGCGCA ACCAGCCCGCG CCGATTGACG TCAATAATGA CCGTATGTTC CATAGTAAAG  
 500 510 520 530 540 550 560  
 CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC TGCCCACTTG GCAGTACATC

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FIG.6B

570 580 590 600 610 620 630  
 AAGIGTATCA TATGCCAAGT ACGCCCCCTA TTGACGTCAA TCAAGGTAAA TGGCCCCGCTT GGCATTATGC  
  
 640 650 660 670 680 690 700  
 CCAGTACATG ACCTTATCGG ACITTTCTAC TTGGCAGTAC ATCTACGTAT TAGTCATCGC TATTACCATG  
  
 710 720 730 740 750 760 770  
 GTGATGCGGT TTTCGCAGTA CATCAATCGG CGTCGATAGC GGTTCAGTC ACGGGGATTT CCAAGICTOC  
  
 780 790 800 810 820 830 840  
 ACCCCATTGA CGTCAATCGG AGTTTGTATT GGCACCACAA TCAACGGGAC TTTCACAAAAT GTCGTACAA  
  
 850 860 870 880 890 900 910  
 CTCGCCCCCA TTGACGCCAA TGGCGCGTAG GCGTGTACGG TGGGAGGCT ATATAAGCAG AGCTCGTTTA  
  
 920 930 940 950 960 970 980  
 GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT TTGACCTCCA TAGAAGACAC CCGGACCGAT  
  
 990 1000 1010 1020 1030 1040 1050  
 CCAGCCTCG CGGCCCGGAA CCGTGCATTG GAACGGGAT TCCCCGIGCC AAGAGTACG TAAGTACCGC  
  
 1060 1070 1080 1090 1100 1110 1120  
 CTATAGACTC TATAGGCACA CCCCCTTGGC TCTTATGCAT GCTATACIGT TTTTGGCTTG GGGCCTATAC

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FIG.6C

1130	1140	1150	1160	1170	1180	1190
ACCCCCCTT	CCCTATGCTA	TAGGICATGG	TATACCTTAG	CCATATAGG	TGGGTTATG	ACCATTTATG
1200	1210	1220	1230	1240	1250	1260
ACCACTCCCC	TATTEGTGAC	GATACCTTTC	ATTACTAATC	CATAACATGG	CTCTTTGGCA	CAACTATCTC
1270	1280	1290	1300	1310	1320	1330
TATTTGGCTAT	ATGCCAATAC	TCCTGTCTTC	ACAGACTGAC	ACGGACTCTG	TATTTTTCAC	GGATGGGGC
1340	1350	1360	1370	1380	1390	1400
CCATTTTATTA	TTTACAAATT	CACATATACA	ACAAGCGCGT	CCCCCGTGCC	CGCAGTTTTT	ATTAAACATA
1410	1420	1430	1440	1450	1460	1470
GGGTGGGATC	TCCACGGGAA	TCCTCGGTAC	GIGTTCGGCA	CATGGGCTCT	TCCTCGGTAG	CGGGCGAGCT
1480	1490	1500	1510	1520	1530	1540
TCCACATCCG	AGCCCTGGTC	CCATGCTTCC	AGCGGCTCAT	GGTGGCTCGG	CAGCTCTCTG	CTCCTAACAG
1550	1560	1570	1580	1590	1600	1610
TGGAGGCCAG	ACTTAGGCAC	AGCACAAATC	CCACCAACAC	CAGGTGCGCG	CACAAGGCCG	TGGCGGTAGG
1620	1630	1640	1650	1660	1670	1680
GTATGTGCT	GAAATGAGC	GTTGAGATTC	GGCTGGCAGC	GCTGACGCAG	ATGGAAGACT	TAAGCCAGCG

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FIG.6D

1690	1700	1710	1720	1730	1740	1750
GCAGAAGAAG	ATGCAGGCAG	CTGAGTGTGT	GTATTTCTGAT	AAGAGTCAGA	GGTAACCTCC	GTTCGGGTGC
1760	1770	1780	1790	1800	1810	1820
TGTTAACGGT	GGAGGGCAGT	GTAGTCTGAG	CAGTACTCGT	TGCTGCGCGG	CGCGCCACCA	GACATAATAG
1830	1840	1850	1860	1870	1880	1890
CTGACAGACT	AACAGACTGT	TOCTTTCCAT	GGGCTTTTC	TGCAGTCACC	GTGTCGACA	CGTGTGATCA
1900	1910	1920	1930	1940	1950	1960
GATAATGCGG	CCGCTCTAGA	CCAGGGCCCT	GGATCCAGAT	CCTGCTGCGC	TTCTAGTTC	CAGCCATCTG
1970	1980	1990	2000	2010	2020	2030
TTGTTTGCCC	CICCCCCGIG	CCTTCTCTCA	CCCTGGAAG	TGCCACTCCC	ACTGTCTTT	CCTAATAAAA
2040	2050	2060	2070	2080	2090	2100
TCAGGAAATT	GCATCGCATT	GCTGAGTAG	GTGTCATCT	ATTCTGCGCG	GTCGGGTGG	GCAGGACAGC
2110	2120	2130	2140	2150	2160	2170
AAGCGGAGG	ATTGGGAAGA	CAATAGCAGG	CATGCTGGCG	ATGGCGTGGG	CTCTATCGGT	ACCCAGGTGC
2180	2190	2200	2210	2220	2230	2240
TGAGAATTG	ACCCGGTTCC	TGCTGGGCCA	GAAAGAAGCA	GGCACATCCC	CTTCTCTGIG	ACACACCCCTG

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FIG.6E

2250 2260 2270 2280 2290 2300 2310  
 TCCAGCCCC TGGTCTTAG TTCCAGCCCC ACTCATAGGA CACTCATAGC TCAGGAGGGC TCCGCCCTTCA  
  
 2320 2330 2340 2350 2360 2370 2380  
 ATCCACCCCG CTAAAGTACT TGGAGCGGTC TTCTCCCTCC TCATCAGCCC ACCAAACCAA ACCTAGCCTC  
  
 2390 2400 2410 2420 2430 2440 2450  
 CAAGAGTCGG AAGAAATTAA AGCAAGATAG GCTATTAAAT GCAGAGGGAG AGAAAAATGCC TCCAACATGT  
  
 2460 2470 2480 2490 2500 2510 2520  
 GAGCAAGTAA TCAGAGAAAT CATAGAAATT CTTCGGCTTC CTGGCTACT GACTCGCTCC GCTCGGTGGT  
  
 2530 2540 2550 2560 2570 2580 2590  
 TCGGCTGGCG CGAGCGGTAT CAGCTCAGTC AAAGCGGGTA ATACGGTTAT CCACAGATC AGGGGATAAC  
  
 2600 2610 2620 2630 2640 2650 2660  
 GCAGGAAAGA ACATGTCAGC AAAAGGCCAG CAAAGGCCA GGAACCGTAA AAAGCGCGG TTGCTGGCGT  
  
 2670 2680 2690 2700 2710 2720 2730  
 TTTTTCATAG GCTCCGCCCC CCCTGACGAGC ATCACAATAA TCGACGCTCA AGTCAGAGGT GCGGAAACCC  
  
 2740 2750 2760 2770 2780 2790 2800  
 GACAGGACTA TAAAGATACC AGCGGTTCOC CCCTGGAAGC TCCCTGGTGC GCCTCTCTGT TCCGACCCCTG

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FIG.6F

2810 2820 2830 2840 2850 2860 2870  
CCGCTTACCG GATACCTGTC CGCCTTCTC CCTTCGGGA GGGGGGGCT TTCTCATAGC TCAAGCTGTA  
2880 2890 2900 2910 2920 2930 2940  
GGTATCTCAG TTCCGGGTAG GTCGTCGCT CCAAGCTGG CTGCTGTCAC GAAACCCCG TTACAGCCGA  
2950 2960 2970 2980 2990 3000 3010  
CCGCTGGCC TTATCCGGTA ACTATCGTCT TGAGTCCAC CCGTAAGAC ACGACTTATC GCCACTGGCA  
3020 3030 3040 3050 3060 3070 3080  
GCAGCCACTG GTAAACAGGAT TAGCAGAGCG AGGTATGTAG GCGTCTTAC AGAGTCTTG AAGTGGTGC  
3090 3100 3110 3120 3130 3140 3150  
CTAACTACCG CTACACTAGA AGAACAGTAT TTGGTATCIG CGCTCTGCTG AAGCCAGTGA CCTTCGGAAA  
3160 3170 3180 3190 3200 3210 3220  
AAGAGTTGGT AGCTCTTGAT CCGGCAACA AACCAACGCT GGTAAGCGIG GTTTTITGT TTGCAAGCAG  
3230 3240 3250 3260 3270 3280 3290  
CAGATTACCG GCAGAAAAA AGGATCTCAA GAAGATCTT TCACTCTTC TACGGGGTCT GAACCTCAGT  
3300 3310 3320 3330 3340 3350 3360  
GGAACGAAA CTAAGCTAA GGGATTTGG TCATGAGAT ATCAAAAAG ATCTTACCT AGATCCTTTT

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FIG.6G

3370 3380 3390 3400 3410 3420 3430  
 AAATTAAAA TGAAGTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCIGACAG TTACCAATGC  
  
 3440 3450 3460 3470 3480 3490 3500  
 TTATTCAGIG AGGCACCTAT CTCAGCGATC TGCTATTTC GTTCATCCAT AGTTGCCCTGA CTCGGGGGGG  
  
 3510 3520 3530 3540 3550 3560 3570  
 GGGGGGCTG AGGCTCGCT CGTGAAGAAG GTGTTCCTGA CTCATACCAG GCTTGAATCG CCCCATCATC  
  
 3580 3590 3600 3610 3620 3630 3640  
 CAGCCAGAAA GTGAGGGAGC CACGGTTGAT GAGAGCTTTC TTGTAGGTGG ACCAGTTGGT GATTHTGAAC  
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 3650 3660 3670 3680 3690 3700 3710  
 TTTTTCCTTG CCACGGAACG GTCTGGGTTG TCGGGAAGAT GGTGATCTG ATCTTCAAC TCAGCAAAAG  
  
 3720 3730 3740 3750 3760 3770 3780  
 TTTCATTAT TCAACAAAGC CGCGTCCCG TCAAGTCAGC GTATGCTCT GCCAGTGTA CAACCAATTA  
  
 3790 3800 3810 3820 3830 3840 3850  
 ACCAATTGIG ATTAGAAAAA CTCATCGAGC ATCAAATGAA ACTGCAATTT ATTCAATATCA GGATTATCAA  
  
 3860 3870 3880 3890 3900 3910 3920  
 TACCATATTT TTGAAAAAGC CGTTTCTGTA ATGAGGAGA AACTCAACG AGCGAGTTC ATAGGATGCG

FIG.6H

3930 3940 3950 3960 3970 3980 3990  
 AATATCCTGG TATCGGICIG CGATTCCGAC TCGICCAACA TCAATACAAC CTATTATATT CCCCCTGICA  
 4000 4010 4020 4030 4040 4050 4060  
 AAAATAAGGT TATCAAGIGA GAAATCACCA TGAGIGACGA CTGAATCCGG TGAGAAATGG AAAAGCTTAT  
 4070 4080 4090 4100 4110 4120 4130  
 GCATTTCCTT CCAGACTTGT TCAACAGGCC AGCCATTAGG CTGICATICA AAATCACCTCG CATCAACCAA  
 4140 4150 4160 4170 4180 4190 4200  
 ACCGTTATTC ATTGCTGATT GCGCCIGAGC GAGACGAAAT ACGCGATCGG TGTATAAAGG ACAATTACAA  
 4210 4220 4230 4240 4250 4260 4270  
 ACAGGAATCG AATGCAACCG GCGCAGGAAC ACTGCCAGCG CATCAACAAT ATTTTCAOCT GAATCAGGAT  
 4280 4290 4300 4310 4320 4330 4340  
 ATTCTTCTAA TACCTGGAAT GCCTGTTTCC CCGCGATCGC AGTGGTGAGT AACCATGCAAT CATCAGGAGT  
 4350 4360 4370 4380 4390 4400 4410  
 ACGGATAAAA TGCCTTGATGG TCGGAAGAGG CATAAATTC GTCAGCCAGT TTAGTCIGAC CATCTCATCT  
 4420 4430 4440 4450 4460 4470 4480  
 GTAACATCAT TGGCAACGCT ACCTTTGCCA TGTTCAGAA ACAACTCIGG CGCATCGGGC TTCCCATACA



FIG.6I

4490 4500 4510 4520 4530 4540 4550  
 ATGATAGAT TGTCGCACCT GATTCGCGCA CATTATCGG AGCCCATTTA TACCCATATA AATCAGCATC  
  
 4560 4570 4580 4590 4600 4610 4620  
 CATGTTGGAA TTTAATCGCG GCGTCGAGCA AGACGTTTCC CGTTCAATAT GGCICATAAC GTTCTTGTGA  
  
 4630 4640 4650 4660 4670 4680 4690  
 TTACIGTTTA TGTAAGCAGA CAGTTTATT GTTCATGATG ATATATTTTT ATCTTGTGCA ATGTAACATC  
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 4700 4710 4720 4730 4740 4750 4760  
 AGAGATTTTG AGACACAAGG TGGCTTTCC CCCCCCCCCA TTATTTGAAGC ATTATCAGG GTTATTGTCT  
  
 4770 4780 4790 4800 4810 4820 4830  
 CATCAGCGCA TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGCGG TTCCGGCCAC ATTTCGCCGA  
  
 4840 4850 4860 4870 4880 4890 4900  
 AAAGTCCAC CTGACGCTA AGAAACCATT ATTATCATGA CATTAACCTA TAAAAATAGG CGTATCAGCA  
  
 4910  
 GGGCTTTTCG TC

FIG. 7

10	20	30	40	50	60	70
CTCCAGTCAC	CGTGGTGGAC	CAGAGCTGAG	ATCCTTACAGG	AGTCCAGGGC	TGGAGAGAAA	ACCTCTGGCA
80	90	100	110	120	130	140
GGAAAGGGAA	GGAGCAAGCC	GTGAATTTAA	GGGACGCTGT	GAAAGCAATCA	TGGATCCCAT	GAAGAGAGGG
150	160	170	180			
CTCTGCTGTC	TGCTGCTGCT	GTGTGGAGCA	GTCTTGGTTT	GGCCCCAGC		

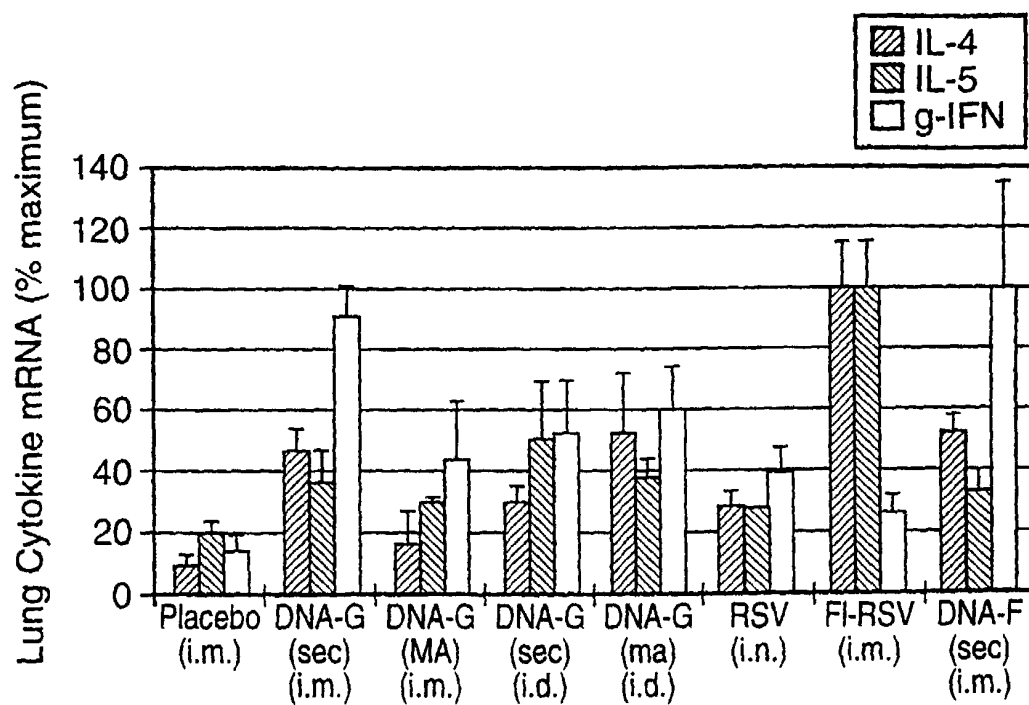


FIG.8